

SEQUENCE LISTING

<110> Moloney, Maurice M.
Van Rooijen, Gijs

<120> Preparation of Heterologous Proteins on Oil Bodies

<130> 9369-292

<150> 09/893,525

<151> 2001-06-29

<150> US 09/210,843

<151> 1998-12-15

<150> US 08/846,021

<151> 1997-04-25

<150> US 08/366,783

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<151> 1993-11-16

<150> US 07/659,835

<151> 1991-02-22

<160> 42

<170> PatentIn version 3.1

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tcgtcgggtc cttgggcat tgcggcggaa gatgggtcag cttgggcttg aggacgagac	180
ccgaatcgag tctgttgaaa ggttgttcat tgggatttgt atacggagat tggctcgtcg	240
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ctctacctc ttccaaaata tatacacatc tttttgatca atctctcatt caaaatctca	840
ttctctctag taaacaagaa caaaaaa atg gcg gat aca gct aga gga acc cat	894
Met Ala Asp Thr Ala Arg Gly Thr His	
1 5	
cac gat atc atc ggc aga gac cag tac ccg atg atg ggc cga gac cga	942
His Asp Ile Ile Gly Arg Asp Gln Tyr Pro Met Met Gly Arg Asp Arg	
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gac cag tac cag atg tcc gga cga gga tct gac tac tcc aag tct agg	990
Asp Gln Tyr Gln Met Ser Gly Arg Gly Ser Asp Tyr Ser Lys Ser Arg	
30 35 40	

cag att gct aaa gct gca act gct gtc aca gct ggt ggt tcc ctc ctt 1038
Gln Ile Ala Lys Ala Ala Thr Ala Val Thr Ala Gly Gly Ser Leu Leu
45 50 55

gtt ctc tcc agc ctt acc ctt gtt gga act gtc ata gct ttg act gtt 1086
Val Leu Ser Ser Leu Thr Leu Val Gly Thr Val Ile Ala Leu Thr Val
60 65 70

gca aca cct ctg ctc gtt atc ttc agc cca atc ctt gtc ccg gct ctc 1134
Ala Thr Pro Leu Leu Val Ile Phe Ser Pro Ile Leu Val Pro Ala Leu
75 80 85

atc aca gtt gca ctc ctc atc acc ggt ttt ctt tcc tct gga ggg ttt 1182
Ile Thr Val Ala Leu Leu Ile Thr Gly Phe Leu Ser Ser Gly Gly Phe
90 95 100 105

ggc att gcc gct ata acc gtt ttc tct tgg att tac aag taagcacaca 1231
Gly Ile Ala Ala Ile Thr Val Phe Ser Trp Ile Tyr Lys
110 115

tttatcatct tacttcataa ttttgtgcaa tatgtgcatg catgtgttga gccagtagct 1291

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aacatttggt taactaaata cgaaatttga cctagctagc ttgaatgtgt ctgtgtatat 1411

catctatata ggtaaaatgc ttggtatgat acctattgat tgtgaatagg tac gca 1467
Tyr Ala
120

acg gga gag cac cca cag gga tca gac aag ttg gac agt gca agg atg 1515
Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala Arg Met
125 130 135

aag ttg gga agc aaa gct cag gat ctg aaa gac aga gct cag tac tac 1563
Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln Tyr Tyr
140 145 150

gga cag caa cat act ggt ggg gaa cat gac cgt gac cgt act cgt ggt 1611
Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr Arg Gly
155 160 165

ggc cag cac act act taa gttacccac tgatgtcatc gtcatagtcc 1659
Gly Gln His Thr Thr
170

aataactcca atgtcgggga gttagtttat gaggaataaaa gtgttttagaa tttgatcagg 1719

gggagataat aaaagccgag tttgaatctt tttgttataa gtaatgttta tgtgtgtttc 1779

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20 25 30

Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
35 40 45

Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu
50 55 60

Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
65 70 75 80

Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
85 90 95

Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
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Phe Ser Trp Ile Tyr Lys
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Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
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35 40 45

Arg Gly Gly Gln His Thr Thr
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<222> (1)..(561)

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tat ccc cga gac cga gac cag tat tct atg atc ggt cga gac cgt gac	96
Tyr Pro Arg Asp Arg Asp Gln Tyr Ser Met Ile Gly Arg Asp Arg Asp	
20 25 30	
cag tac tct atg atg ggc cga gac cga gac cag tac aac atg tat ggt	144
Gln Tyr Ser Met Met Gly Arg Asp Arg Asp Gln Tyr Asn Met Tyr Gly	
35 40 45	
cga gac tac tcc aag tct aga cag att gct aag gct gtt acc gca gtc	192
Arg Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Val Thr Ala Val	
50 55 60	
acg gcg ggt ggg tcc ctc ctt gtc ctc tcc agt ctc acc ctt gtt ggt	240
Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val Gly	
65 70 75 80	
act gtc att gct ttg act gtt gcc act cca ctc ctc gtt atc ttt agc	288
Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe Ser	
85 90 95	
cca atc ctc gtg ccg gct ctc atc acc gta gca ctt ctc atc act ggc	336
Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr Gly	
100 105 110	
ttt ctc tcc tct ggt ggg ttt gcc att gca gct ata acc gtc ttc tcc	384
Phe Leu Ser Ser Gly Gly Phe Ala Ile Ala Ala Ile Thr Val Phe Ser	
115 120 125	
tgg atc tat aag tac gca acg gga gag cac cca cag ggg tca gat aag	432
Trp Ile Tyr Lys Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys	
130 135 140	
ttg gac agt gca agg atg aag ctg gga acc aaa gct cag gat att aaa	480
Leu Asp Ser Ala Arg Met Lys Leu Gly Thr Lys Ala Gln Asp Ile Lys	
145 150 155 160	
gac aga gct caa tac tac gga cag caa cat aca ggt ggt gag cat gac	528
Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp	
165 170 175	
cgt gac cgt act cgt ggt ggc cag cac act act taa	564
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Gln Tyr Ser Met Met Gly Arg Asp Arg Asp Gln Tyr Asn Met Tyr Gly
35 40 45

Arg Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Val Thr Ala Val
50 55 60

Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val Gly
65 70 75 80

Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe Ser
85 90 95

Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr Gly
100 105 110

Phe Leu Ser Ser Gly Gly Phe Ala Ile Ala Ala Ile Thr Val Phe Ser
115 120 125

Trp Ile Tyr Lys Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys
130 135 140

Leu Asp Ser Ala Arg Met Lys Leu Gly Thr Lys Ala Gln Asp Ile Lys
145 150 155 160

Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp
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Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr
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<222> (850) .. (1203)

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cacgtgactt ctogtctcct ttcttaatat atctaacaaa cactcctacc tcttccaaaa	780
tatatacaca tctttttgat caatctctca ttcaaaatct cattctctct agtaaacaag	840
aacaaaaaa atg gcg gat aca gct aga gga acc cat cac gat atc atc ggc	891
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aga gac cag tac ccg atg atg ggc cga gac cga gac cag tac cag atg	939
Arg Asp Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met	
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tcc gga cga gga tct gac tac tcc aag tct agg cag att gct aaa gct	987
Ser Gly Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala	
35 40 45	

gca act gct gtc aca gct ggt ggt tcc ctc ctt gtt ctc tcc agc ctt	1035
Ala Thr Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu	
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acc ctt gtt gga act gtc ata gct ttg act gtt gca aca cct ctg ctc	1083
Thr Leu Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu	
65 70 75	
gtt atc ttc agc cca atc ctt gtc ccg gct ctc atc aca gtt gca ctc	1131
Val Ile Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu	
80 85 90	
ctc atc acc ggt ttt ctt tcc tct gga ggg ttt ggc att gcc gct ata	1179
Leu Ile Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile	
95 100 105 110	
acc gtt ttc tct tgg att tac aag taagcacaca tttatcatct tacttcataa	1233
Thr Val Phe Ser Trp Ile Tyr Lys	
115	
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Tyr Ala Thr Gly Glu His Pro Gln	
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gga tca gac aag ttg gac agt gca agg atg aag ttg gga agc aaa gct	1515
Gly Ser Asp Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala	
130 135 140	
cag gat ctg aaa gac aga gct cag tac tac gga cag caa cat act ggt	1563
Gln Asp Leu Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly	
145 150 155	
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Gly Glu His Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr Leu	
160 165 170	
gtt cca cga gga tcc atg gct gag atc acc agg atc cct ctg tac aaa	1659
Val Pro Arg Gly Ser Met Ala Glu Ile Thr Arg Ile Pro Leu Tyr Lys	
175 180 185 190	
ggc aag tct ctg agg aag gcg ctg aag gag cat ggg ctt ctg gag gac	1707
Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu Leu Glu Asp	
195 200 205	
ttc ctg cag aaa cag cag tat ggc atc agc agc aag tac tcc ggc ttc	1755
Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr Ser Gly Phe	
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Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp Ser Gln Tyr	
225 230 235	
ttt ggg aag atc tac ctc ggg acc ccg ccc cag gag ttc acc gtg ctg	1851
Phe Gly Lys Ile Tyr Leu Thr Pro Pro Gln Glu Phe Thr Val Leu	
240 245 250	
ttt gac act ggc tcc tct gac ttc tgg gta ccc tct atc tac tgc aag	1899
Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile Tyr Cys Lys	
255 260 265 270	

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Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg Lys Ser Ser	
275 280 285	
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Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr Gly Thr Gly	
290 295 300	
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Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val Ser Asn Ile	
305 310 315	
gtg gac atc cag cag aca gta ggc ctg agc acc cag gag ccc ggg gac	2091
Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu Pro Gly Asp	
320 325 330	
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Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met Ala Tyr Pro	
335 340 345 350	
tcg ctc gcc tca gag tac tcg ata ccc gtg ttt gac aac atg atg aac	2187
Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn Met Met Asn	
355 360 365	
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Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met Asp Arg Asn	
370 375 380	
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Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro Ser Tyr Tyr	
385 390 395	
aca ggg tcc ctg cac tgg gtg ccc gtg aca gtg cag cag tac tgg cag	2331
Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln Tyr Trp Gln	
400 405 410	
ttc act gtg gac agt gtc acc atc agc ggt gtg gtt gtg gcc tgt gag	2379
Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val Ala Cys Glu	
415 420 425 430	
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Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys Leu Val Gly	
435 440 445	
ccc agc agc gac atc ctc aac atc cag cag gcc att gga gcc aca cag	2475
Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly Ala Thr Gln	
450 455 460	
aac cag tac ggt gag ttt gac atc gac tgc gac aac ctg agc tac atg	2523
Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu Ser Tyr Met	
465 470 475	
ccc act gtg gtc ttt gag atc aat ggc aaa atg tac cca ctg acc ccc	2571
Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro Leu Thr Pro	
480 485 490	
tcc gcc tat acc agc caa gac cag ggc ttc tgt acc agt ggc ttc cag	2619
Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser Gly Phe Gln	
495 500 505 510	
agt gaa aat cat tcc cag aaa tgg atc ctg ggg gat gtt ttc atc cga	2667
Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val Phe Ile Arg	
515 520 525	
gag tat tac agc gtc ttt gac agg gcc aac aac ctc gtg ggg ctg gcc	2715

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Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val Gly Leu Ala
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2733

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<212> PRT

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<223> Oleosin-Chymosin Fusion

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Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
35 40 45

Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu
50 55 60

Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
65 70 75 80

Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
85 90 95

Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
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Phe Ser Trp Ile Tyr Lys
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<212> PRT

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20 25 30

Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
35 40 45

Arg Gly Gly Gln His Thr Thr Leu Val Pro Arg Gly Ser Met Ala Glu
50 55 60

Ile Thr Arg Ile Pro Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu
65 70 75 80

Lys Glu His Gly Leu Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly
85 90 95

Ile Ser Ser Lys Tyr Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu
100 105 110

Thr Asn Tyr Leu Asp Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr
115 120 125

Pro Pro Gln Glu Phe Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe
130 135 140

Trp Val Pro Ser Ile Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln
145 150 155 160

Arg Phe Asp Pro Arg Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro
165 170 175

Leu Ser Ile His Tyr Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr
180 185 190

Asp Thr Val Thr Val Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly
195 200 205

Leu Ser Thr Gln Glu Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp
210 215 220

Gly Ile Leu Gly Met Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile
225 230 235 240

- 95 -

Pro Val Phe Asp Asn Met Met Asn Arg His Leu Val Ala Gln Asp Leu
245 250 255

Phe Ser Val Tyr Met Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu
260 265 270

Gly Ala Ile Asp Pro Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro
275 280 285

Val Thr Val Gln Gln Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile
290 295 300

Ser Gly Val Val Val Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp
305 310 315 320

Thr Gly Thr Ser Lys Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile
325 330 335

Gln Gln Ala Ile Gly Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile
340 345 350

Asp Cys Asp Asn Leu Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn
355 360 365

Gly Lys Met Tyr Pro Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln
370 375 380

Gly Phe Cys Thr Ser Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp
385 390 395 400

Ile Leu Gly Asp Val Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg
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<223> Factor Xa Cleavage Site

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<223> Collagenase Cleavage Site

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<212> DNA

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<223> ALP1 Primer

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tc 62

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<212> DNA

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<223> Primer GVR20

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<210> 21

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Leu Val Pro Arg Gly Ser
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<223> IL-1-B Peptide

<400> 22

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<210> 23

<211> 28

<212> DNA

<213> Artificial Sequence

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37

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<223> 5'-Bam-Oleo

<400> 27

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<211> 22

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<211> 738

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<212> DNA

<213> Artificial Sequence

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<223> Phas-GUS-phas

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caccaaacia tcatttggtg tatttctgaa gcaagtcctg ttatgcaaaa ttctataatt	660
cccatttgac actacggaag taactgaaga tctgctttta catgcgagac acatcttcta	720
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	Met Val Leu
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Arg Pro Val Glu Thr Pro Thr Arg Glu Ile Lys Lys Leu Asp Gly Leu	
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Trp Ala Phe Ser Leu Asp Arg Glu Asn Cys Gly Ile Asp Gln Arg Trp	
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Trp Glu Ser Ala Leu Gln Glu Ser Arg Ala Ile Ala Val Pro Gly Ser	
40 45 50	
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Phe Asn Asp Gln Phe Ala Asp Ala Asp Ile Arg Asn Tyr Ala Gly Asn	
55 60 65	
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Val Trp Tyr Gln Arg Glu Val Phe Ile Pro Lys Gly Trp Ala Gly Gln	
70 75 80	
cgt atc gtg ctg cgt ttc gat gcg gtc act cat tac ggc aaa gtg tgg	1844
Arg Ile Val Leu Arg Phe Asp Ala Val Thr His Tyr Gly Lys Val Trp	
85 90 95	
gtc aat aat cag gaa gtg atg gag cat cag ggc ggc tat acg cca ttt	1892
Val Asn Asn Gln Glu Val Met Glu His Gln Gly Gly Tyr Thr Pro Phe	
100 105 110 115	
gaa gcc gat gtc acg ccg tat gtt att gcc ggg aaa agt gta cgt atc	1940
Glu Ala Asp Val Thr Pro Tyr Val Ile Ala Gly Lys Ser Val Arg Ile	
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acc gtt tgt gtg aac aac gaa ctg aac tgg cag act atc ccg ccg gga	1988
Thr Val Cys Val Asn Asn Glu Leu Asn Trp Gln Thr Ile Pro Pro Gly	
135 140 145	
atg gtg att acc gac gaa aac ggc aag aaa aag cag tct tac ttc cat	2036
Met Val Ile Thr Asp Glu Asn Gly Lys Lys Lys Gln Ser Tyr Phe His	
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gat ttc ttt aac tat gcc gga atc cat cgc agc gta atg ctc tac acc	2084
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165 170 175	
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Thr Pro Asn Thr Trp Val Asp Asp Ile Thr Val Val Thr His Val Ala	
180 185 190 195	
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Gln Asp Cys Asn His Ala Ser Val Asp Trp Gln Val Val Ala Asn Gly	
200 205 210	
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Asp Val Ser Val Glu Leu Arg Asp Ala Asp Gln Gln Val Val Ala Thr	
215 220 225	

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gca gtg aag ggc caa cag ttc ctg att aac cac aaa ccg ttc tac ttt Ala Val Lys Gly Gln Gln Phe Leu Ile Asn His Lys Pro Phe Tyr Phe 280 285 290	2420
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gat aac gtg ctg atg gtg cac gac cac gca tta atg gac tgg att ggg Asp Asn Val Leu Met Val His Asp His Ala Leu Met Asp Trp Ile Gly 310 315 320	2516
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gcg cac tta cag gcg att aaa gag ctg ata gcg cgt gac aaa aac cac Ala His Leu Gln Ala Ile Lys Glu Leu Ile Ala Arg Asp Lys Asn His 390 395 400	2756
cca agc gtg gtg atg tgg agt att gcc aac gaa ccg gat acc cgt ccg Pro Ser Val Val Met Trp Ser Ile Ala Asn Glu Pro Asp Thr Arg Pro 405 410 415	2804
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gct cac acc gat acc atc agc gat ctc ttt gat gtg ctg tgc ctg aac Ala His Thr Asp Thr Ile Ser Asp Leu Phe Asp Val Leu Cys Leu Asn 455 460 465	2948
cgt tat tac gga tgg tat gtc caa agc ggc gat ttg gaa acg gca gag Arg Tyr Tyr Gly Trp Tyr Val Gln Ser Gly Asp Leu Glu Thr Ala Glu 470 475 480	2996
aag gta ctg gaa aaa gaa ctt ctg gcc tgg cag gag aaa ctg cat cag Lys Val Leu Glu Lys Glu Leu Leu Ala Trp Gln Glu Lys Leu His Gln	3044

485	490	495	
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cag gta tgg aat ttc gcc gat ttt gcg acc tcg caa ggc ata ttg cgc Gln Val Trp Asn Phe Ala Asp Phe Ala Thr Ser Gln Gly Ile Leu Arg 550 555 560			3236
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tcg gcg gct ttt ctg ctg caa aaa cgc tgg act ggc atg aac ttc ggt Ser Ala Ala Phe Leu Gln Lys Arg Trp Thr Gly Met Asn Phe Gly 580 585 590 595			3332
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<212> PRT

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<400> 37

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35 40 45

Pro Gly Ser Phe Asn Asp Gln Phe Ala Asp Ala Asp Ile Arg Asn Tyr
50 55 60

Ala Gly Asn Val Trp Tyr Gln Arg Glu Val Phe Ile Pro Lys Gly Trp
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Ala Gly Gln Arg Ile Val Leu Arg Phe Asp Ala Val Thr His Tyr Gly
85 90 95

Lys Val Trp Val Asn Asn Gln Glu Val Met Glu His Gln Gly Gly Tyr
100 105 110

Thr Pro Phe Glu Ala Asp Val Thr Pro Tyr Val Ile Ala Gly Lys Ser
115 120 125

Val Arg Ile Thr Val Cys Val Asn Asn Glu Leu Asn Trp Gln Thr Ile
130 135 140

Pro Pro Gly Met Val Ile Thr Asp Glu Asn Gly Lys Lys Lys Gln Ser
145 150 155 160

Tyr Phe His Asp Phe Phe Asn Tyr Ala Gly Ile His Arg Ser Val Met

165	170	175
Leu Tyr Thr Thr Pro Asn Thr Trp Val Asp Asp Ile Thr Val Val Thr		
180	185	190
His Val Ala Gln Asp Cys Asn His Ala Ser Val Asp Trp Gln Val Val		
195	200	205
Ala Asn Gly Asp Val Ser Val Glu Leu Arg Asp Ala Asp Gln Gln Val		
210	215	220
Val Ala Thr Gly Gln Gly Thr Ser Gly Thr Leu Gln Val Val Asn Pro		
225	230	235
His Leu Trp Gln Pro Gly Glu Gly Tyr Leu Tyr Glu Leu Cys Val Thr		
245	250	255
Ala Lys Ser Gln Thr Glu Cys Asp Ile Tyr Pro Leu Arg Val Gly Ile		
260	265	270
Arg Ser Val Ala Val Lys Gly Gln Gln Phe Leu Ile Asn His Lys Pro		
275	280	285
Phe Tyr Phe Thr Gly Phe Gly Arg His Glu Asp Ala Asp Leu Arg Gly		
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Lys Gly Phe Asp Asn Val Leu Met Val His Asp His Ala Leu Met Asp		
305	310	315
Trp Ile Gly Ala Asn Ser Tyr Arg Thr Ser His Tyr Pro Tyr Ala Glu		
325	330	335
Glu Met Leu Asp Trp Ala Asp Glu His Gly Ile Val Val Ile Asp Glu		
340	345	350
Thr Ala Ala Val Gly Phe Ser Leu Ser Leu Gly Ile Gly Phe Glu Ala		
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Gly Asn Lys Pro Lys Glu Leu Tyr Ser Glu Glu Ala Val Asn Gly Glu		
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Thr Gln Gln Ala His Leu Gln Ala Ile Lys Glu Leu Ile Ala Arg Asp		
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Lys Asn His Pro Ser Val Val Met Trp Ser Ile Ala Asn Glu Pro Asp		
405	410	415
Thr Arg Pro Gln Gly Ala Arg Glu Tyr Phe Ala Pro Leu Ala Glu Ala		
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Thr Arg Lys Leu Asp Pro Thr Arg Pro Ile Thr Cys Val Asn Val Met
435 440 445

Phe Cys Asp Ala His Thr Asp Thr Ile Ser Asp Leu Phe Asp Val Leu
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Cys Leu Asn Arg Tyr Tyr Gly Trp Tyr Val Gln Ser Gly Asp Leu Glu
465 470 475 480

Thr Ala Glu Lys Val Leu Glu Lys Glu Leu Leu Ala Trp Gln Glu Lys
485 490 495

Leu His Gln Pro Ile Ile Ile Thr Glu Tyr Gly Val Asp Thr Leu Ala
500 505 510

Gly Leu His Ser Met Tyr Thr Asp Met Trp Ser Glu Glu Tyr Gln Cys
515 520 525

Ala Trp Leu Asp Met Tyr His Arg Val Phe Asp Arg Val Ser Ala Val
530 535 540

Val Gly Glu Gln Val Trp Asn Phe Ala Asp Phe Ala Thr Ser Gln Gly
545 550 555 560

Ile Leu Arg Val Gly Gly Asn Lys Lys Gly Ile Phe Thr Arg Asp Arg
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<222> (1555)..(1908)

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<222> (2149)..(4125)

<223>

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agtttaaagt aaatataagt aatgtagtag agtgtagtag tgttacccta aaccataaac	960
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Met	

1

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gga tct gac tac tcc aag tct agg cag att gct aaa gct gca act gct Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr Ala 35 40 45	1701
gtc aca gct ggt ggt tcc ctc ctt gtt ctc tcc agc ctt acc ctt gtt Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val 50 55 60 65	1749
gga act gtc ata gct ttg act gtt gca aca cct ctg ctc gtt atc ttc Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe 70 75 80	1797
agc cca atc ctt gtc ccg gct ctc atc aca gtt gca ctc ctc atc acc Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr 85 90 95	1845
ggg ttt ctt tcc tct gga ggg ttt ggc att gcc gct ata acc gtt ttc Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val Phe 100 105 110	1893
tct tgg att tac aag taagcacaca tttatcatct tacttcataa tttgtgcaa Ser Trp Ile Tyr Lys 115	1948
tatgtgcatg catgtgttga gccagtagct ttggatcaat ttttttggtc gaataacaaa	2008
tgtaaacaata agaaattgca aattctaggg aacatttggg taactaaata cgaaatttga	2068
cctagctagc ttgaatgtgt ctgtgtatat catctatata ggtaaaatgc ttggtatgat	2128
acctattgat tgtgaatagg tac gca acg gga gag cac cca cag gga tca gac Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp 120 125	2181
aag ttg gac agt gca agg atg aag ttg gga agc aaa gct cag gat ctg Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu 130 135 140 145	2229
aaa gac aga gct cag tac tac gga cag caa cat act ggt ggg gaa cat Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His 150 155 160	2277
gac cgt gac cgt act cgt ggt ggc cag cac act acc atg gtc tta cgt Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr Met Val Leu Arg 165 170 175	2325
cct gta gaa acc cca acc cgt gaa atc aaa aaa ctc gac ggc ctg tgg Pro Val Glu Thr Pro Thr Arg Glu Ile Lys Lys Leu Asp Gly Leu Trp 180 185 190	2373
gca ttc agt ctg gat cgc gaa aac tgt gga att gat cag cgt tgg tgg Ala Phe Ser Leu Asp Arg Glu Asn Cys Gly Ile Asp Gln Arg Trp Trp 195 200 205	2421
gaa agc gcg tta caa gaa agc cgg gca att gct gtg cca ggc agt ttt Glu Ser Ala Leu Gln Glu Ser Arg Ala Ile Ala Val Pro Gly Ser Phe	2469

210	215	220	225	
aac gat cag ttc gcc gat gca gat att cgt aat tat gcg ggc aac gtc				2517
Asn Asp Gln Phe Ala Asp Ala Asp Ile Arg Asn Tyr Ala Gly Asn Val	230	235	240	
tgg tat cag cgc gaa gtc ttt ata ccg aaa ggt tgg gca ggc cag cgt				2565
Trp Tyr Gln Arg Glu Val Phe Ile Pro Lys Gly Trp Ala Gly Gln Arg	245	250	255	
atc gtg ctg cgt ttc gat gcg gtc act cat tac ggc aaa gtg tgg gtc				2613
Ile Val Leu Arg Phe Asp Ala Val Thr His Tyr Gly Lys Val Trp Val	260	265	270	
aat aat cag gaa gtg atg gag cat cag ggc ggc tat acg cca ttt gaa				2661
Asn Asn Gln Glu Val Met Glu His Gln Gly Gly Tyr Thr Pro Phe Glu	275	280	285	
gcc gat gtc acg ccg tat gtt att gcc ggg aaa agt gta cgt atc acc				2709
Ala Asp Val Thr Pro Tyr Val Ile Ala Gly Lys Ser Val Arg Ile Thr	290	295	300	305
gtt tgt gtg aac aac gaa ctg aac tgg cag act atc ccg ccg gga atg				2757
Val Cys Val Asn Asn Glu Leu Asn Trp Gln Thr Ile Pro Pro Gly Met	310	315	320	
gtg att acc gac gaa aac ggc aag aaa aag cag tct tac ttc cat gat				2805
Val Ile Thr Asp Glu Asn Gly Lys Lys Lys Gln Ser Tyr Phe His Asp	325	330	335	
ttc ttt aac tat gcc gga atc cat cgc agc gta atg ctc tac acc acg				2853
Phe Phe Asn Tyr Ala Gly Ile His Arg Ser Val Met Leu Tyr Thr Thr	340	345	350	
ccg aac acc tgg gtg gac gat atc acc gtg gtg acg cat gtc gcg caa				2901
Pro Asn Thr Trp Val Asp Asp Ile Thr Val Val Thr His Val Ala Gln	355	360	365	
gac tgt aac cac gcg tct gtt gac tgg cag gtg gtg gcc aat ggt gat				2949
Asp Cys Asn His Ala Ser Val Asp Trp Gln Val Val Ala Asn Gly Asp	370	375	380	385
gtc agc gtt gaa ctg cgt gat gcg gat caa cag gtg gtt gca act gga				2997
Val Ser Val Glu Leu Arg Asp Ala Asp Gln Gln Val Val Ala Thr Gly	390	395	400	
caa ggc act agc ggg act ttg caa gtg gtg aat ccg cac ctc tgg caa				3045
Gln Gly Thr Ser Gly Thr Leu Gln Val Val Asn Pro His Leu Trp Gln	405	410	415	
ccg ggt gaa ggt tat ctc tat gaa ctg tgc gtc aca gcc aaa agc cag				3093
Pro Gly Glu Gly Tyr Leu Tyr Glu Leu Cys Val Thr Ala Lys Ser Gln	420	425	430	
aca gag tgt gat atc tac ccg ctt cgc gtc ggc atc cgg tca gtg gca				3141
Thr Glu Cys Asp Ile Tyr Pro Leu Arg Val Gly Ile Arg Ser Val Ala	435	440	445	
gtg aag ggc caa cag ttc ctg att aac cac aaa ccg ttc tac ttt act				3189
Val Lys Gly Gln Gln Phe Leu Ile Asn His Lys Pro Phe Tyr Phe Thr	450	455	460	465
ggc ttt ggt cgt cat gaa gat gcg gac tta cgt ggc aaa gga ttc gat				3237
Gly Phe Gly Arg His Glu Asp Ala Asp Leu Arg Gly Lys Gly Phe Asp	470	475	480	

aac gtg ctg atg gtg cac gac cac gca tta atg gac tgg att ggg gcc	3285
Asn Val Leu Met Val His Asp His Ala Leu Met Asp Trp Ile Gly Ala	
485 490 495	
aac tcc tac cgt acc tcg cat tac cct tac gct gaa gag atg ctc gac	3333
Asn Ser Tyr Arg Thr Ser His Tyr Pro Tyr Ala Glu Glu Met Leu Asp	
500 505 510	
tgg gca gat gaa cat ggc atc gtg gtg att gat gaa act gct gct gtc	3381
Trp Ala Asp Glu His Gly Ile Val Val Ile Asp Glu Thr Ala Ala Val	
515 520 525	
ggc ttt tcg ctc tct tta ggc att ggt ttc gaa gcg ggc aac aag ccg	3429
Gly Phe Ser Leu Ser Leu Gly Ile Gly Phe Glu Ala Gly Asn Lys Pro	
530 535 540 545	
aaa gaa ctg tac agc gaa gag gca gtc aac ggg gaa act cag caa gcg	3477
Lys Glu Leu Tyr Ser Glu Glu Ala Val Asn Gly Glu Thr Gln Gln Ala	
550 555 560	
cac tta cag gcg att aaa gag ctg ata gcg cgt gac aaa aac cac cca	3525
His Leu Gln Ala Ile Lys Glu Leu Ile Ala Arg Asp Lys Asn His Pro	
565 570 575	
agc gtg gtg atg tgg agt att gcc aac gaa ccg gat acc cgt ccg caa	3573
Ser Val Val Met Trp Ser Ile Ala Asn Glu Pro Asp Thr Arg Pro Gln	
580 585 590	
ggt gca cgg gaa tat ttc gcg cca ctg gcg gaa gca acg cgt aaa ctc	3621
Gly Ala Arg Glu Tyr Phe Ala Pro Leu Ala Glu Ala Thr Arg Lys Leu	
595 600 605	
gac ccg acg cgt ccg atc acc tgc gtc aat gta atg ttc tgc gac gct	3669
Asp Pro Thr Arg Pro Ile Thr Cys Val Asn Val Met Phe Cys Asp Ala	
610 615 620 625	
cac acc gat acc atc agc gat ctc ttt gat gtg ctg tgc ctg aac cgt	3717
His Thr Asp Thr Ile Ser Asp Leu Phe Asp Val Leu Cys Leu Asn Arg	
630 635 640	
tat tac gga tgg tat gtc caa agc ggc gat ttg gaa acg gca gag aag	3765
Tyr Tyr Gly Trp Tyr Val Gln Ser Gly Asp Leu Glu Thr Ala Glu Lys	
645 650 655	
gta ctg gaa aaa gaa ctt ctg gcc tgg cag gag aaa ctg cat cag ccg	3813
Val Leu Glu Lys Glu Leu Leu Ala Trp Gln Glu Lys Leu His Gln Pro	
660 665 670	
att atc atc acc gaa tac ggc gtg gat acg tta gcc ggg ctg cac tca	3861
Ile Ile Ile Thr Glu Tyr Gly Val Asp Thr Leu Ala Gly Leu His Ser	
675 680 685	
atg tac acc gac atg tgg agt gaa gag tat cag tgt gca tgg ctg gat	3909
Met Tyr Thr Asp Met Trp Ser Glu Glu Tyr Gln Cys Ala Trp Leu Asp	
690 695 700 705	
atg tat cac cgc gtc ttt gat cgc gtc agc gcc gtc gtc ggt gaa cag	3957
Met Tyr His Arg Val Phe Asp Arg Val Ser Ala Val Val Gly Glu Gln	
710 715 720	
gta tgg aat ttc gcc gat ttt gcg acc tcg caa ggc ata ttg cgc gtt	4005
Val Trp Asn Phe Ala Asp Phe Ala Thr Ser Gln Gly Ile Leu Arg Val	
725 730 735	
ggc ggt aac aag aaa ggg atc ttc act cgc gac cgc aaa ccg aag tcg	4053
Gly Gly Asn Lys Lys Gly Ile Phe Thr Arg Asp Arg Lys Pro Lys Ser	

740	745	750	
gcg gct ttt ctg ctg caa aaa cgc tgg act ggc atg aac ttc ggt gaa			4101
Ala Ala Phe Leu Leu Gln Lys Arg Trp Thr Gly Met Asn Phe Gly Glu			
755	760	765	
aaa ccg cag cag gga ggc aaa caa tgaatcaaca actctcctgg cgcaccatcg			4155
Lys Pro Gln Gln Gly Gly Lys Gln			
770	775		
tcggctacag cctcgggtgga attcgatatc aagcttaaata aagtatgaac taaaatgcat			4215
gtaggtgtaa gagctcatgg agagcatgga atattgtatc cgaccatgta acagtataat			4275
aactgagctc catctcactt cttctatgaa taaacaaagg atgttatgat atattaacac			4335
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cactatatga aatttttttt ttttatcggc aaggaaataa aattaaatta ggagggacaa			5115
tggtgtgtcc caatccttat acaaccaact tccacaggaa ggtcaggctg gggacaacaa			5175
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gtaaaacact acacataacc ctttttagcag tagagcaatg gttgaccgtg tgcttagctt			5295
cttttatttt atttttttat cagcaaagaa taaataaaat aaaatgagac acttcagga			5355
tgtttcaacc cttatacaaa accccaaaaa caagtttctt agcaccctac caactaaggt			5415
acc			5418

<210> 39

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> phas-oleo GUS-phas

<400> 39

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Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly
20 25 30

Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
35 40 45

Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu
50 55 60

Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
65 70 75 80

Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
85 90 95

Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
100 105 110

Phe Ser Trp Ile Tyr Lys
115

<210> 40

<211> 659

<212> PRT

<213> Artificial Sequence

<220>

<223> phas-oleo GUS-phas

<400> 40

Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
1 5 10 15

Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
20 25 30

Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
35 40 45

Arg Gly Gly Gln His Thr Thr Met Val Leu Arg Pro Val Glu Thr Pro

50						55						60					
Thr	Arg	Glu	Ile	Lys	Lys	Leu	Asp	Gly	Leu	Trp	Ala	Phe	Ser	Leu	Asp		
65					70					75					80		
Arg	Glu	Asn	Cys	Gly	Ile	Asp	Gln	Arg	Trp	Trp	Glu	Ser	Ala	Leu	Gln		
				85					90					95			
Glu	Ser	Arg	Ala	Ile	Ala	Val	Pro	Gly	Ser	Phe	Asn	Asp	Gln	Phe	Ala		
			100					105					110				
Asp	Ala	Asp	Ile	Arg	Asn	Tyr	Ala	Gly	Asn	Val	Trp	Tyr	Gln	Arg	Glu		
		115					120					125					
Val	Phe	Ile	Pro	Lys	Gly	Trp	Ala	Gly	Gln	Arg	Ile	Val	Leu	Arg	Phe		
	130					135					140						
Asp	Ala	Val	Thr	His	Tyr	Gly	Lys	Val	Trp	Val	Asn	Asn	Gln	Glu	Val		
145					150					155				160			
Met	Glu	His	Gln	Gly	Gly	Tyr	Thr	Pro	Phe	Glu	Ala	Asp	Val	Thr	Pro		
				165					170					175			
Tyr	Val	Ile	Ala	Gly	Lys	Ser	Val	Arg	Ile	Thr	Val	Cys	Val	Asn	Asn		
			180					185					190				
Glu	Leu	Asn	Trp	Gln	Thr	Ile	Pro	Pro	Gly	Met	Val	Ile	Thr	Asp	Glu		
		195					200					205					
Asn	Gly	Lys	Lys	Lys	Gln	Ser	Tyr	Phe	His	Asp	Phe	Phe	Asn	Tyr	Ala		
	210					215					220						
Gly	Ile	His	Arg	Ser	Val	Met	Leu	Tyr	Thr	Thr	Pro	Asn	Thr	Trp	Val		
225					230					235				240			
Asp	Asp	Ile	Thr	Val	Val	Thr	His	Val	Ala	Gln	Asp	Cys	Asn	His	Ala		
				245					250					255			
Ser	Val	Asp	Trp	Gln	Val	Val	Ala	Asn	Gly	Asp	Val	Ser	Val	Glu	Leu		
		260						265					270				
Arg	Asp	Ala	Asp	Gln	Gln	Val	Val	Ala	Thr	Gly	Gln	Gly	Thr	Ser	Gly		
		275					280					285					
Thr	Leu	Gln	Val	Val	Asn	Pro	His	Leu	Trp	Gln	Pro	Gly	Glu	Gly	Tyr		
	290					295					300						
Leu	Tyr	Glu	Leu	Cys	Val	Thr	Ala	Lys	Ser	Gln	Thr	Glu	Cys	Asp	Ile		
305					310					315				320			

Tyr Pro Leu Arg Val Gly Ile Arg Ser Val Ala Val Lys Gly Gln Gln
325 330 335

Phe Leu Ile Asn His Lys Pro Phe Tyr Phe Thr Gly Phe Gly Arg His
340 345 350

Glu Asp Ala Asp Leu Arg Gly Lys Gly Phe Asp Asn Val Leu Met Val
355 360 365

His Asp His Ala Leu Met Asp Trp Ile Gly Ala Asn Ser Tyr Arg Thr
370 375 380

Ser His Tyr Pro Tyr Ala Glu Glu Met Leu Asp Trp Ala Asp Glu His
385 390 395 400

Gly Ile Val Val Ile Asp Glu Thr Ala Ala Val Gly Phe Ser Leu Ser
405 410 415

Leu Gly Ile Gly Phe Glu Ala Gly Asn Lys Pro Lys Glu Leu Tyr Ser
420 425 430

Glu Glu Ala Val Asn Gly Glu Thr Gln Gln Ala His Leu Gln Ala Ile
435 440 445

Lys Glu Leu Ile Ala Arg Asp Lys Asn His Pro Ser Val Val Met Trp
450 455 460

Ser Ile Ala Asn Glu Pro Asp Thr Arg Pro Gln Gly Ala Arg Glu Tyr
465 470 475 480

Phe Ala Pro Leu Ala Glu Ala Thr Arg Lys Leu Asp Pro Thr Arg Pro
485 490 495

Ile Thr Cys Val Asn Val Met Phe Cys Asp Ala His Thr Asp Thr Ile
500 505 510

Ser Asp Leu Phe Asp Val Leu Cys Leu Asn Arg Tyr Tyr Gly Trp Tyr
515 520 525

Val Gln Ser Gly Asp Leu Glu Thr Ala Glu Lys Val Leu Glu Lys Glu
530 535 540

Leu Leu Ala Trp Gln Glu Lys Leu His Gln Pro Ile Ile Ile Thr Glu
545 550 555 560

Tyr Gly Val Asp Thr Leu Ala Gly Leu His Ser Met Tyr Thr Asp Met
565 570 575

Trp Ser Glu Glu Tyr Gln Cys Ala Trp Leu Asp Met Tyr His Arg Val

	580		585		590
Phe Asp Arg Val Ser Ala Val Val Gly Glu Gln Val Trp Asn Phe Ala	595		600		605
Asp Phe Ala Thr Ser Gln Gly Ile Leu Arg Val Gly Gly Asn Lys Lys	610		615		620
Gly Ile Phe Thr Arg Asp Arg Lys Pro Lys Ser Ala Ala Phe Leu Leu	625		630		635
Gln Lys Arg Trp Thr Gly Met Asn Phe Gly Glu Lys Pro Gln Gln Gly		645		650	655
Gly Lys Gln					

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<211> 5390

<212> DNA

<213> Artificial Sequence

<220>

<223> phas-caleo-GUS-phas

<220>

<221> CDS

<222> (1548) .. (4097)

<223>

<400> 41

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gttactttaa tttctcataa tctttggttg aaattatcac gcttccgcac acgatatccc	180
tacaaattta ttatttggtta aacattttca aaccgcataa aattttatga agtcccgctt	240
atctttaatg tagtctaaca ttttcatatt gaaatatata atttacttaa ttttagcggt	300
ggtagaaaagc ataaagattt attcttattc ttcttcatat aaatgtttta tatacaatat	360
aaacaaattc tttaccttaa gaaggatttc ccattttata ttttaaaaat atatttatca	420
aatatttttc aaccacgtaa atctcataat aataagttgt ttcaaaagta ataaaattta	480
actccataat ttttttattc gactgatctt aaagcaacac ccagtgcac aactagccat	540

ttttttcttt gaataaaaaa atccaattat cattgtattt tttttataca atgaaaattt	600
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cccatttgac actacggaag taactgaaga tctgctttta catgcgagac acatcttcta	720
aagtaatttt aataatagtt actatattca agatttcata tatcaaatac tcaatattac	780
ttctaaaaaa ttaattagat ataattaaaa tattactttt ttaattttta gtttaattgt	840
tgaatttgtg actattgatt tattattcta ctatgtttta attgttttat agatagttta	900
aagtaaatat aagtaatgta gtagagtgtt agagtgttac cctaaacat aaactataac	960
atztatgggtg gactaatttt catatatattc ttattgcttt taccttttct tggtagtaa	1020
gtccgtaact agaattacag tgggttgcca tgacactctg tggctctttg gttcatgcat	1080
gggtcttgcg caagaaaaag acaagaaca aagaaaaaag acaaacaga gagacaaac	1140
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caaccacac acaaacacat tgctttttc ttcatcatca ccacaaccac ctgtatatat	1320
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taaatactc taatatcact cacttctttc atcatccatc catccagagt actactactc	1500
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	Met Gly Ser
	1
aag acg gag atg atg gag aga gac gca atg gct acg gtg gct ccc tat	1604
Lys Thr Glu Met Met Glu Arg Asp Ala Met Ala Thr Val Ala Pro Tyr	
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gcg ccg gtc act tac cac cgc cgt gct cgt gtt gac ttg gat gat aga	1652
Ala Pro Val Thr Tyr His Arg Arg Ala Arg Val Asp Leu Asp Asp Arg	
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Leu Pro Lys Pro Tyr Met Pro Arg Ala Leu Gln Ala Pro Asp Arg Glu	
40 45 50	
cac ccg tac gga act cca ggc cat aag aat tac gga ctt agt gtt ctt	1748
His Pro Tyr Gly Thr Pro Gly His Lys Asn Tyr Gly Leu Ser Val Leu	
55 60 65	
caa cag cat gtc tcc ttc ttc gat atc gat gat aat ggc atc att tac	1796
Gln Gln His Val Ser Phe Phe Asp Ile Asp Asp Asn Gly Ile Ile Tyr	
70 75 80	
cct tgg gag acc tac tct gga ctg cga atg ctt ggt ttc aat atc att	1844
Pro Trp Glu Thr Tyr Ser Gly Leu Arg Met Leu Gly Phe Asn Ile Ile	
85 90 95	
ggg tcg ctt ata ata gcc gct gtt atc aac ctg acc ctt agc tat gcc	1892
Gly Ser Leu Ile Ile Ala Ala Val Ile Asn Leu Thr Leu Ser Tyr Ala	
100 105 110 115	
act ctt ccg ggg tgg tta cct tca cct ttc ttc cct ata tac ata cac	1940
Thr Leu Pro Gly Trp Leu Pro Ser Pro Phe Phe Pro Ile Tyr Ile His	

				120				125				130					
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gaa Glu	gga Gly	agg Arg 150	ttt Phe	atg Met	ccg Pro	gtg Val	aat Asn 155	ctt Leu	gag Glu	ttg Leu	ata Ile	ttt Phe 160	agc Ser	aaa Lys	tat Tyr	2036	
gcg Ala	aaa Lys 165	acc Thr	ttg Leu	cca Pro	gac Asp	aag Lys 170	ttg Leu	agt Ser	ctt Leu	gga Gly	gaa Glu 175	cta Leu	tgg Trp	gag Glu	atg Met	2084	
aca Thr 180	gaa Glu	gga Gly	aac Asn	cgt Arg	gac Asp 185	gct Ala	tgg Trp	gac Asp	att Ile	ttt Phe 190	gga Gly	tgg Trp	atc Ile	gca Ala	ggc Gly 195	2132	
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gag Glu	tac Tyr	tgt Cys 230	gcc Ala	aaa Lys	atc Ile	tac Tyr	gct Ala 235	ggt Gly	atc Ile	agt Ser	gaa Glu	gac Asp 240	aag Lys	aca Thr	gca Ala	2276	
tac Tyr	tac Tyr 245	gcc Ala	atg Met	gtc Val	tta Leu	cgt Arg 250	cct Pro	gta Val	gaa Glu	acc Thr	cca Pro 255	acc Thr	cgt Arg	gaa Glu	atc Ile	2324	
aaa Lys 260	aaa Lys	ctc Leu	gac Asp	ggc Gly 265	ctg Leu	tgg Trp	gca Ala	ttc Phe	agt Ser	ctg Leu 270	gat Asp	cgc Arg	gaa Glu	aac Asn	tgt Cys 275	2372	
gga Gly	att Ile	gat Asp	cag Gln	cgt Arg 280	tgg Trp	tgg Trp	gaa Glu	agc Ser	gcg Ala 285	tta Leu	caa Gln	gaa Glu	agc Ser	cgg Arg 290	gca Ala	2420	
att Ile	gct Ala	gtg Val	cca Pro 295	ggc Gly	agt Ser	ttt Phe	aac Asn	gat Asp 300	cag Gln	ttc Phe	gcc Ala	gat Asp 305	gca Ala	gat Asp	att Ile	2468	
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645	650	655	
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aat gta atg ttc tgc gac gct cac acc gat acc atc agc gat ctc ttt Asn Val Met Phe Cys Asp Ala His Thr Asp Thr Ile Ser Asp Leu Phe 695 700 705			3668
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Asp Asp Arg Leu Pro Lys Pro Tyr Met Pro Arg Ala Leu Gln Ala Pro
35 40 45

Asp Arg Glu His Pro Tyr Gly Thr Pro Gly His Lys Asn Tyr Gly Leu
50 55 60

Ser Val Leu Gln Gln His Val Ser Phe Phe Asp Ile Asp Asp Asn Gly
65 70 75 80

Ile Ile Tyr Pro Trp Glu Thr Tyr Ser Gly Leu Arg Met Leu Gly Phe

- 125 -

	85		90		95										
Asn	Ile	Ile	Gly	Ser	Leu	Ile	Ile	Ala	Ala	Val	Ile	Asn	Leu	Thr	Leu
			100					105					110		
Ser	Tyr	Ala	Thr	Leu	Pro	Gly	Trp	Leu	Pro	Ser	Pro	Phe	Phe	Pro	Ile
		115					120					125			
Tyr	Ile	His	Asn	Ile	His	Lys	Ser	Lys	His	Gly	Ser	Asp	Ser	Lys	Thr
	130					135					140				
Tyr	Asp	Asn	Glu	Gly	Arg	Phe	Met	Pro	Val	Asn	Leu	Glu	Leu	Ile	Phe
145					150					155					160
Ser	Lys	Tyr	Ala	Lys	Thr	Leu	Pro	Asp	Lys	Leu	Ser	Leu	Gly	Glu	Leu
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Trp	Glu	Met	Thr	Glu	Gly	Asn	Arg	Asp	Ala	Trp	Asp	Ile	Phe	Gly	Trp
			180					185					190		
Ile	Ala	Gly	Lys	Ile	Glu	Trp	Gly	Leu	Leu	Tyr	Leu	Leu	Ala	Arg	Asp
		195					200					205			
Glu	Glu	Gly	Phe	Leu	Ser	Lys	Glu	Ala	Ile	Arg	Arg	Cys	Phe	Asp	Gly
	210					215					220				
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Lys	Thr	Ala	Tyr	Tyr	Ala	Met	Val	Leu	Arg	Pro	Val	Glu	Thr	Pro	Thr
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Arg	Glu	Ile	Lys	Lys	Leu	Asp	Gly	Leu	Trp	Ala	Phe	Ser	Leu	Asp	Arg
			260					265					270		
Glu	Asn	Cys	Gly	Ile	Asp	Gln	Arg	Trp	Trp	Glu	Ser	Ala	Leu	Gln	Glu
		275					280					285			
Ser	Arg	Ala	Ile	Ala	Val	Pro	Gly	Ser	Phe	Asn	Asp	Gln	Phe	Ala	Asp
	290					295					300				
Ala	Asp	Ile	Arg	Asn	Tyr	Ala	Gly	Asn	Val	Trp	Tyr	Gln	Arg	Glu	Val
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Phe	Ile	Pro	Lys	Gly	Trp	Ala	Gly	Gln	Arg	Ile	Val	Leu	Arg	Phe	Asp
				325					330					335	
Ala	Val	Thr	His	Tyr	Gly	Lys	Val	Trp	Val	Asn	Asn	Gln	Glu	Val	Met
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Glu His Gln Gly Gly Tyr Thr Pro Phe Glu Ala Asp Val Thr Pro Tyr
355 360 365

Val Ile Ala Gly Lys Ser Val Arg Ile Thr Val Cys Val Asn Asn Glu
370 375 380

Leu Asn Trp Gln Thr Ile Pro Pro Gly Met Val Ile Thr Asp Glu Asn
385 390 395 400

Gly Lys Lys Lys Gln Ser Tyr Phe His Asp Phe Phe Asn Tyr Ala Gly
405 410 415

Ile His Arg Ser Val Met Leu Tyr Thr Thr Pro Asn Thr Trp Val Asp
420 425 430

Asp Ile Thr Val Val Thr His Val Ala Gln Asp Cys Asn His Ala Ser
435 440 445

Val Asp Trp Gln Val Val Ala Asn Gly Asp Val Ser Val Glu Leu Arg
450 455 460

Asp Ala Asp Gln Gln Val Val Ala Thr Gly Gln Gly Thr Ser Gly Thr
465 470 475 480

Leu Gln Val Val Asn Pro His Leu Trp Gln Pro Gly Glu Gly Tyr Leu
485 490 495

Tyr Glu Leu Cys Val Thr Ala Lys Ser Gln Thr Glu Cys Asp Ile Tyr
500 505 510

Pro Leu Arg Val Gly Ile Arg Ser Val Ala Val Lys Gly Gln Gln Phe
515 520 525

Leu Ile Asn His Lys Pro Phe Tyr Phe Thr Gly Phe Gly Arg His Glu
530 535 540

Asp Ala Asp Leu Arg Gly Lys Gly Phe Asp Asn Val Leu Met Val His
545 550 555 560

Asp His Ala Leu Met Asp Trp Ile Gly Ala Asn Ser Tyr Arg Thr Ser
565 570 575

His Tyr Pro Tyr Ala Glu Glu Met Leu Asp Trp Ala Asp Glu His Gly
580 585 590

Ile Val Val Ile Asp Glu Thr Ala Ala Val Gly Phe Ser Leu Ser Leu
595 600 605

Gly Ile Gly Phe Glu Ala Gly Asn Lys Pro Lys Glu Leu Tyr Ser Glu

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Glu Ala Val Asn Gly 625	Glu Thr Gln Gln Ala His 630	Leu Gln Ala Ile Lys 635
Glu Leu Ile Ala Arg 645	Asp Lys Asn His 650	Pro Ser Val Val Met Trp Ser 655
Ile Ala Asn Glu Pro Asp Thr Arg 660	Pro Gln Gly Ala Arg 665	Glu Tyr Phe 670
Ala Pro Leu Ala Glu Ala Thr Arg 675	Lys Leu Asp Pro Thr Arg Pro Ile 680	
Thr Cys Val Asn Val Met Phe Cys Asp Ala His Thr Asp Thr Ile Ser 690		700
Asp Leu Phe Asp Val Leu Cys Leu Asn Arg Tyr Tyr Gly Trp Tyr Val 705		715
Gln Ser Gly Asp Leu Glu Thr Ala Glu Lys Val Leu Glu Lys Glu Leu 725		730
Leu Ala Trp Gln Glu Lys Leu His Gln Pro Ile Ile Ile Thr Glu Tyr 740		745
Gly Val Asp Thr Leu Ala Gly Leu His Ser Met Tyr Thr Asp Met Trp 755		760
Ser Glu Glu Tyr Gln Cys Ala Trp Leu Asp Met Tyr His Arg Val Phe 770		775
Asp Arg Val Ser Ala Val Val Gly Glu Gln Val Trp Asn Phe Ala Asp 785		790
Phe Ala Thr Ser Gln Gly Ile Leu Arg Val Gly Gly Asn Lys Lys Gly 805		810
Ile Phe Thr Arg Asp Arg Lys Pro Lys Ser Ala Ala Phe Leu Leu Gln 820		825
Lys Arg Trp Thr Gly Met Asn Phe Gly Glu Lys Pro Gln Gln Gly Gly 835		840
Lys Gln 850		